

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/915,543

DATE: 11/16/2001

TIME: 08:29:01

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Output Set: N:\CRF3\11162001\I915543.raw

ENTERED

3 <110> APPLICANT: BASLER, Konrad
4 BRUNNER, Erich
5 FROESCH, Barbara
6 KRAMPS, Thomas
7 PETER, Oliver
9 <120> TITLE OF INVENTION: ESSENTIAL DOWNSTREAM COMPONENT OF THE WINGLESS SIGNALING
PATHWAY AND
10 THERAPEUTIC AND DIAGNOSTIC APPLICATIONS BASED THEREON
12 <130> FILE REFERENCE: Q60361
14 <140> CURRENT APPLICATION NUMBER: 09/915,543
15 <141> CURRENT FILING DATE: 2001-07-27
17 <150> PRIOR APPLICATION NUMBER: 60/221,502
18 <151> PRIOR FILING DATE: 2000-07-28
20 <160> NUMBER OF SEQ ID NOS: 22
22 <170> SOFTWARE: PatentIn version 3.1
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26 <212> TYPE: DNA
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70 ttagcttaat acgatgtctc gaagtgttat tgcatttgca catatacata aaattgtgac 180
72 atagaatagg agaattccac atacaaatac aaaaatacaa aatcctccag taaaatttaa 240

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78 agcaataaaa cgatggattt taattgctac ttgagcaatt agccacacaa gggatcttgg 420
80 gaaggtcgat ttgaaggaat tcgatttcta ggatgctctc gacaaca atg ccc cgc 476
81                                     Met Pro Arg
82                                     1
84 agt cca acc caa caa cag ccg caa cca aac tcc gat gcc tcc tca aca 524
85 Ser Pro Thr Gln Gln Gln Pro Gln Pro Asn Ser Asp Ala Ser Ser Thr
86   5                               10                               15
88 agt gca tct gga tca aat cct gga gca gcg atc gga aat ggg gac tcg 572
89 Ser Ala Ser Gly Ser Asn Pro Gly Ala Ala Ile Gly Asn Gly Asp Ser
90 20                               25                               30                               35
92 gcg gcg agc aga agt tct ccg aag acc ctt aat agc gaa ccc ttt tct 620
93 Ala Ala Ser Arg Ser Ser Pro Lys Thr Leu Asn Ser Glu Pro Phe Ser
94   40                               45                               50
96 act ttg tcg ccg ggtaagactt gtattgattt ctctttgtcc ggaattataa 672
97 Thr Leu Ser Pro
98   55
100 caactttctg tgtttcca gat caa ata aaa ttg acg cca gaa gaa ggc act 723
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102                                     60                                     65
104 gag aaa agc gga cta tca act agt gat aaa gct gcc act gga gga gcc 771
105 Glu Lys Ser Gly Leu Ser Thr Ser Asp Lys Ala Ala Thr Gly Gly Ala
106   70                               75                               80
108 cca ggc agt gga aat aat ctg ccc gag gga caa act atg cta agg cag 819
109 Pro Gly Ser Gly Asn Asn Leu Pro Glu Gly Gln Thr Met Leu Arg Gln
110   85                               90                               95
112 aac tct acg agc aca atc aac tcg tgc cta gtc gct tct cca caa aac 867
113 Asn Ser Thr Ser Thr Ile Asn Ser Cys Leu Val Ala Ser Pro Gln Asn
114   100                               105                               110
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117 Ser Ser Glu His Ser Asn Ser Ser Asn Val Ser Ala Thr Val Gly Leu
118 115                               120                               125                               130
120 act cag atg gta gat tgt gac gag caa tcg aag aaa aac aaa tgt agt 963
121 Thr Gln Met Val Asp Cys Asp Glu Gln Ser Lys Lys Asn Lys Cys Ser
122   135                               140                               145
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142 cataaccatt aatgtcccat ttca gaa ata agt tct aat aaa gca aaa ggt 1482
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150  gtc aag gaa gaa ccc acc gat gtc tta ggc agt tta gta aat atg aaa      1578
151  Val Lys Glu Glu Pro Thr Asp Val Leu Gly Ser Leu Val Asn Met Lys
152                180          185          190
154  aaa gaa gaa aga gaa aat cat tcg cca acg atg tcc cct gtt ggt ttt      1626
155  Lys Glu Glu Arg Glu Asn His Ser Pro Thr Met Ser Pro Val Gly Phe
156                195          200          205
158  ggt tca att ggt aat gca cag gac aac tcc gct aca ccg ggtaagtttt      1675
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160  210                215          220
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164  tcaaagaact actatagcga tatctcctgc cttttaattt tattttaatt aggaaatag      1795
166  aatattttcta atttgtaaaa taaaattgat taattaacta gaatttaaaa accttttgaa      1855
168  ttaggacata cccttccaaa aatcagtaat cattgggaac gagagtgtgg tcccgaagga      1915
170  gactactata aaaccttttg agctatctga tactgcacgc tactaaaaat gattagttta      1975
172  ggaaaaatggg tgtaattttg taggaagttt tcattttaga agaaatgtga ttattttatt      2035
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178  aattttgatt aaatgagaaa ttatcacact tcagttaaaa tgtttaattc gattaaggtc      2215
180  ggacaatcac agcagatttc catttttgcg tgtatatata gaagtcgcct tcacactctt      2275
182  ctggcgcgct tcaccactac gtggagttcc gccgcagtg atttatatag atgatttacg      2335
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186  gtt aaa att gaa aga att tca aac gac agt acc acg gaa aaa aaa gga      2441
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190  tcg tcc ttg aca atg aat aat gac gaa atg agc atg gaa ggc tgc aat      2489
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192                240          245          250
194  cag ttg aat ccc gat ttt atc aat gaa tct tta aat aat cct gca att      2537
195  Gln Leu Asn Pro Asp Phe Ile Asn Glu Ser Leu Asn Asn Pro Ala Ile
196  255                260          265          270
198  tcg agc ata tta gta agc gga gta gga cca ata ccc gga atc gga gtt      2585
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202  gga gcg ggg acg gga aat tta ttg act gcc aac gcc aat gga atc tcc      2633
203  Gly Ala Gly Thr Gly Asn Leu Leu Thr Ala Asn Ala Asn Gly Ile Ser
204                290          295          300
206  tcg ggt agc agt aat tgt ttg gat tac atg caa cag caa aat cac ata      2681
207  Ser Gly Ser Ser Asn Cys Leu Asp Tyr Met Gln Gln Gln Asn His Ile
208                305          310          315
210  ttc gtg ttt tca act cag ctg gcc aac aaa ggg gcc gaa tca gtt tta      2729
211  Phe Val Phe Ser Thr Gln Leu Ala Asn Lys Gly Ala Glu Ser Val Leu
212                320          325          330
214  agc ggt caa ttt caa act att att gcg tat cac tgc act cag cct gct      2777
215  Ser Gly Gln Phe Gln Thr Ile Ile Ala Tyr His Cys Thr Gln Pro Ala
216  335                340          345          350
218  aca aaa agc ttc ctg gaa gac ttt ttt atg aaa aac cct tta aag att      2825

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226	ggg	cag	gtt	gga	cta	act	cct	cct	aat	cct	gta	gcc	aaa	ata	aca	caa	2921
227	Gly	Gln	Val	Gly	Leu	Thr	Pro	Pro	Asn	Pro	Val	Ala	Lys	Ile	Thr	Gln	
228			385					390					395				
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232		400					405					410					
234	caa	cat	gaa	aac	agc	aaa	cgt	agt	act	gta	agc	gcg	cct	agc	aac	tct	3017
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242	tgg	gaa	ggc	gga	tcc	tca	aac	acc	agt	agg	tct	gga	caa	aac	tca	cga	3113
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254	gat	cct	ggc	ctg	aca	act	gaa	aac	aac	att	gta	tca	ctg	caa	gga	gtt	3257
255	Asp	Pro	Gly	Leu	Thr	Thr	Glu	Asn	Asn	Ile	Val	Ser	Leu	Gln	Gly	Val	
256	495				500					505					510		
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259	Lys	Val	Pro	Asp	Glu	Asn	Leu	Thr	Pro	Gln	Gln	Arg	Gln	His	Arg	Glu	
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262	gaa	cag	ttg	gca	aaa	ata	aaa	aaa	atg	aat	caa	ttt	ctt	ttt	cct	gaa	3353
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266	aat	gag	aat	tca	gta	gga	gct	aat	gta	agc	tca	cag	ata	aca	aaa	att	3401
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271	Pro	Gly	Asp	Leu	Met	Met	Gly	Met	Ser	Gly	Gly	Gly	Gly	Gly	Ser	Ile	
272		560				565					570						
274	ata	aat	ccg	acg	atg	cga	caa	ctg	cat	atg	cca	ggg	aac	gcc	aaa	tcg	3497
275	Ile	Asn	Pro	Thr	Met	Arg	Gln	Leu	His	Met	Pro	Gly	Asn	Ala	Lys	Ser	
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278	gag	ctc	tta	tcg	gcg	aca	agt	tca	gga	ctt	tcg	gaa	gat	gta	atg	cat	3545
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288	625																630																635																																
290	gga	aca	act	gca	gct	gga	gta	aat	gtc	aat	atg	cat	tgc	tca	agc	tcc	3689																																																
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300	675																680																685																																
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320	755																760																765																																
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323	Arg	Ser	Ala	Ser	Val	Pro	Ile	Ala	Thr	Gln	Ser	Pro	Asn	Pro	Ser	Ser																																																	
324	770																775																780																																
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